

FIGURE 1

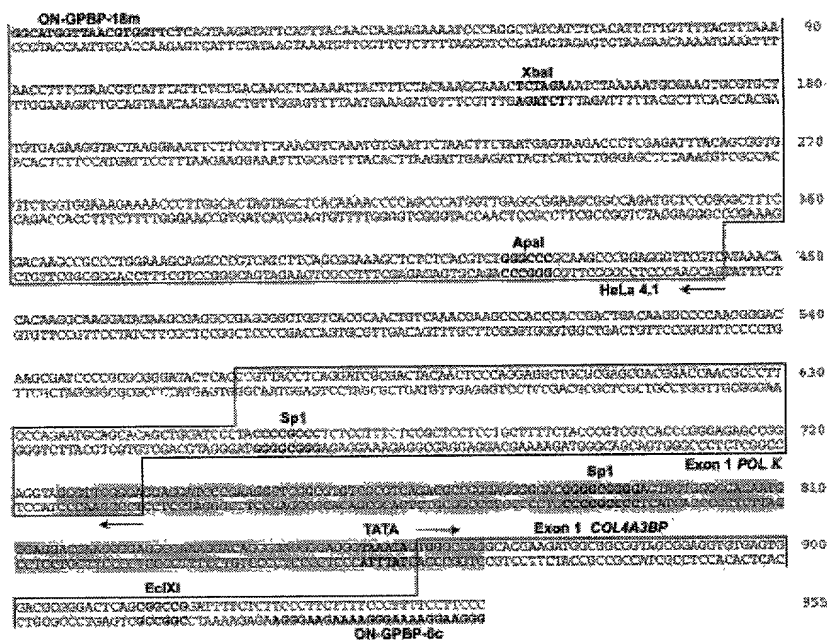


FIGURE 2

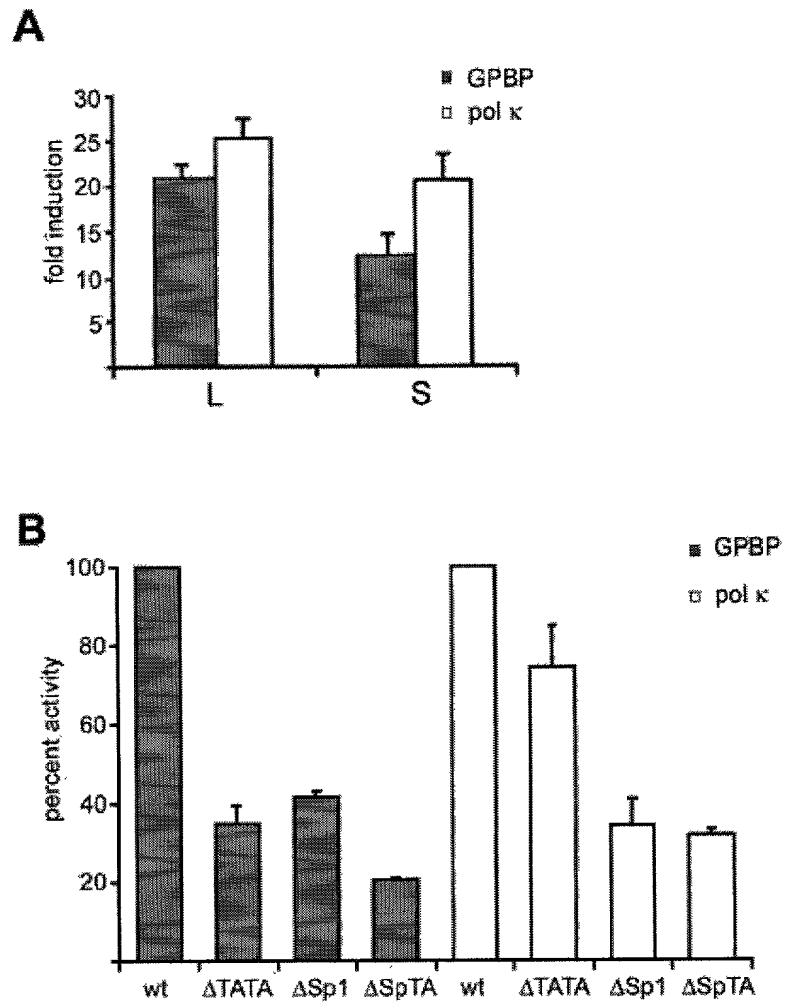
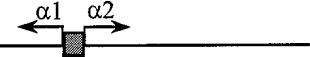
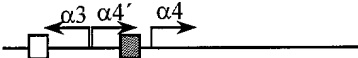
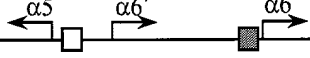


FIGURE 3

	<i>COL4A3BP</i> ■	<i>POLK</i> □	Alignment map*
<i>COL4A1-A2</i> ($\alpha_1\alpha_2$) GenBank no M36963	Region aligned 469-608 $Q=620$; $E(Q)=591.4\pm17.1$ $z=1.6725$, $P=0.00472$	Region aligned 583-722 $Q=580$; $E(Q)=571\pm19$ $z=0.4737$, $P=0.3179$	
<i>COL4A3-A4</i> ($\alpha_3\alpha_4$) GenBank no. AF218541	Region aligned 849-990 $Q=674$; $E(Q)=568.7\pm17.5$ $z=6.0171$, $P<0.0001$	Region aligned 182-318 $Q=641$; $E(Q)=557.5\pm18.4$ $z=4.5380$, $P<0.0001$	
<i>COL4A5-A6</i> ($\alpha_5\alpha_6$) GenBank no D28116	Region aligned 1714-1853 $Q=570$; $E(Q)=524.2\pm18.4$ $z=2.4891$, $P=0.0064$	Region aligned 440-579 $Q=570$; $E(Q)=527.4\pm17.3$ $z=2.4624$, $P=0.0069$	

Q is a measure of the quality of the alignment.

$E(Q)$ is the Q value expected by chance.

z -score for Q . This score is normally distributed with mean zero and variance 1.

P is the probability of observing Q just by chance.

*In the drawing (————— ~ 0.5 kb) are indicated the statistically significant alignments (P values in *boldface*).

10000721-120701

FIGURE 4

	<i>COL4A3BP</i> ■	<i>POLK</i> □	Alignment map*
<i>LMP2-TAP1</i>	Region aligned 24579-24718	Region aligned 27355-27494	
GenBank no. X66401	$Q=610$; $E(Q)=549.9 \pm 16.9$ $z=3.5562$, $P=0.0002$	$Q=620$; $E(Q)=582.8 \pm 18.6$ $z=2$, $P=0.0228$	
<i>MRP1-DHFR</i>	Region aligned 849-991	Region aligned 704-843	
GenBank no. K01612	$Q=581$; $E(Q)=557.7 \pm 20.8$ $z=1.1202$, $P=0.1313$	$Q=640$; $E(Q)=553.4 \pm 18.1$ $z=4.7845$, $P<0.0001$	
<i>GPAT-AIRC</i>	Region aligned 632-769	Region aligned 561-705	
GenBank no. U00239	$Q=554$; $E(Q)=573.4 \pm 20.4$ $z=-0.9510$, $P=0.8292$	$Q=565$; $E(Q)=549.4 \pm 18.4$ $z=0.8478$, $P=0.1983$	
<i>HO3-HRS</i>	Region aligned 313-452	Region aligned 214-353	
GenBank no. M96646	$Q=600$; $E(Q)=531 \pm 17.5$ $z=3.9429$, $P<0.0001$	$Q=560$; $E(Q)=557.1 \pm 16.2$ $z=0.1790$, $P=0.4290$	
<i>HSP10-HSP60</i>	Region aligned 3451-3590	Region aligned 3684-3821	
GenBank no. AJ250915	$Q=600$; $E(Q)=546.7 \pm 16.7$ $z=3.1916$, $P=0.0007$	$Q=594$; $E(Q)=542.6 \pm 17.1$ $z=3.0058$, $P=0.0013$	
<i>IDHG-TRAPD</i>	Region aligned 16283-16422	Region aligned 14190-14329	
GenBank no. Z68129	$Q=622$; $E(Q)=594.8 \pm 16.5$ $z=2.7394$, $P=0.0031$	$Q=610$; $E(Q)=601.9 \pm 15.5$ $z=0.5226$, $P=0.3006$	

Q is a measure of the quality of the alignment.

$E(Q)$ is the Q value expected by chance.

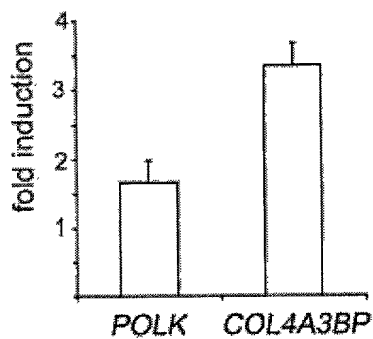
z -score for Q . This score is normally distributed with mean zero and variance 1.

P is the probability of observing Q just by chance.

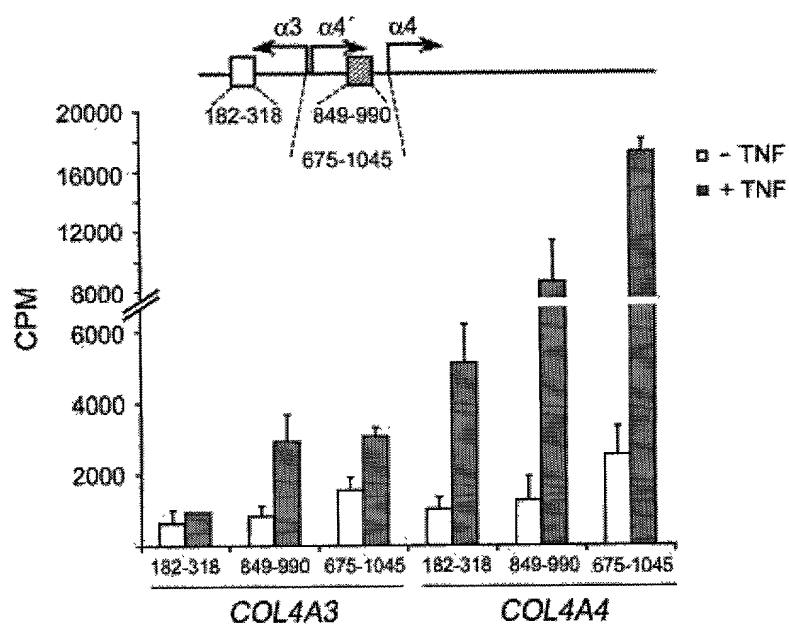
*In the drawing (■ ~ 0.5 kb) are indicated the significant alignments (P values in *boldface*).

FIGURE 5

A



B



C

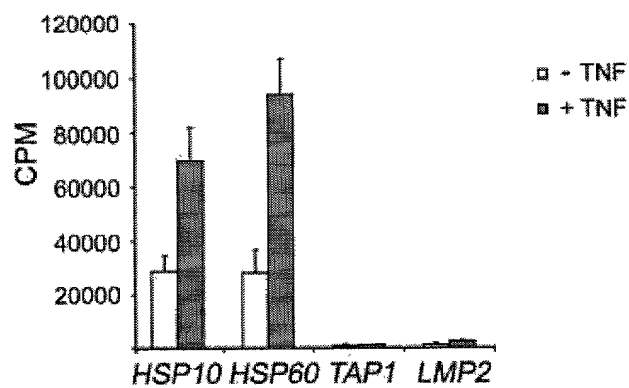


FIGURE 6

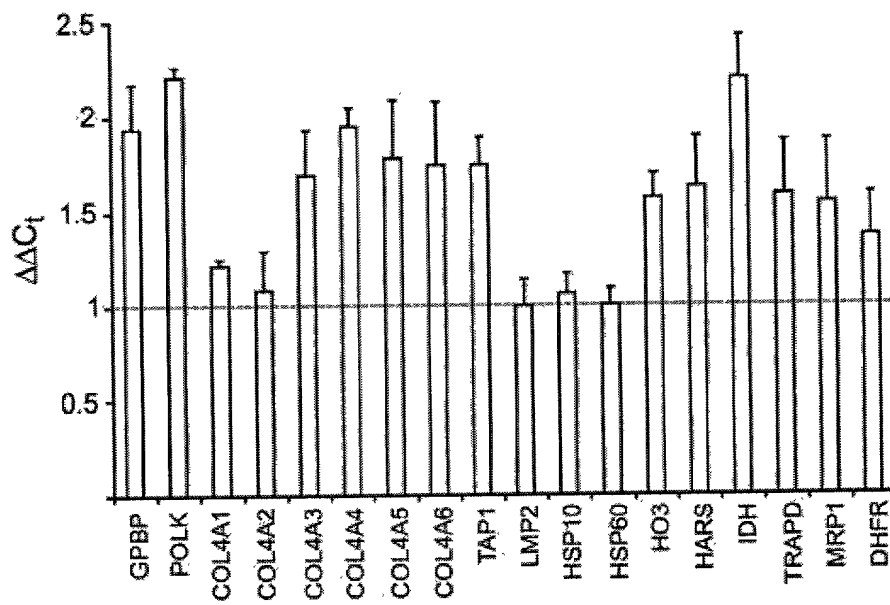


FIGURE 7

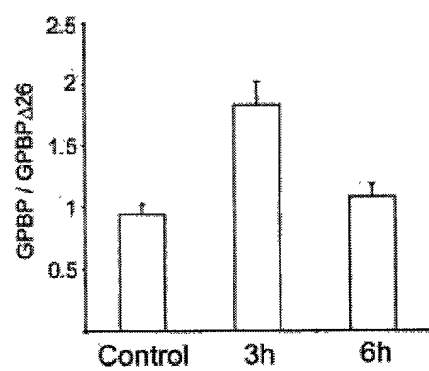
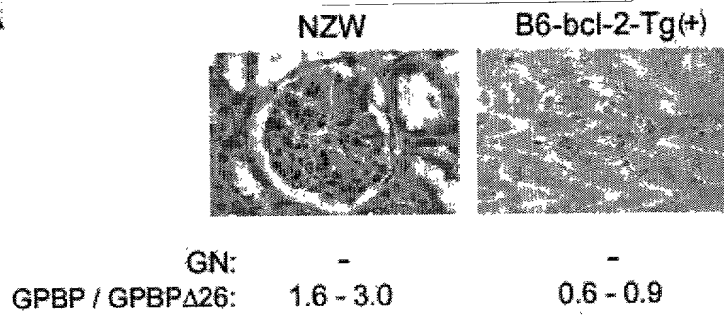
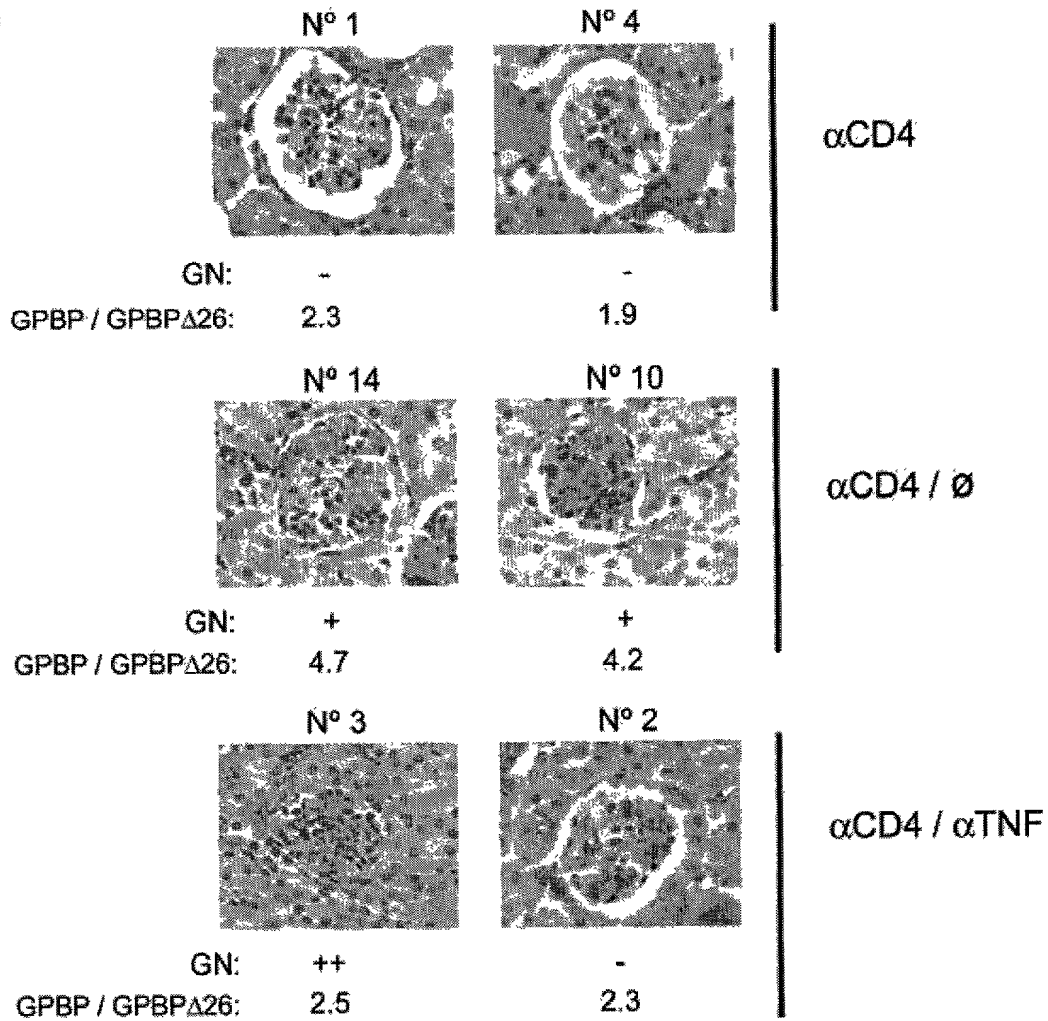


FIGURE 8

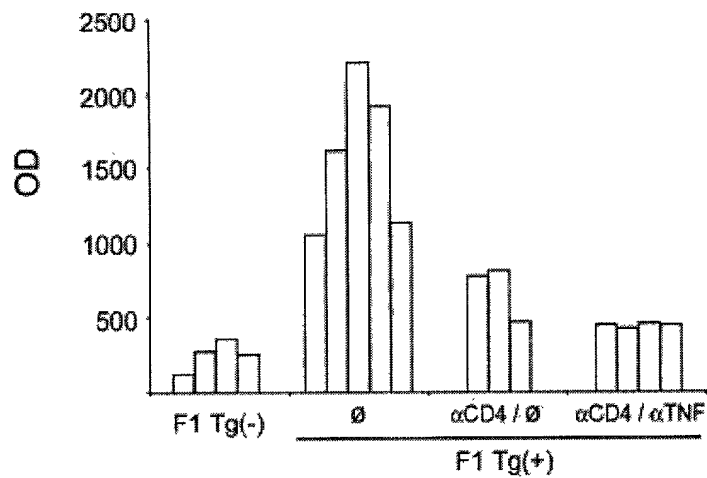
A



B



C



10006724.130704

FIGURE 9

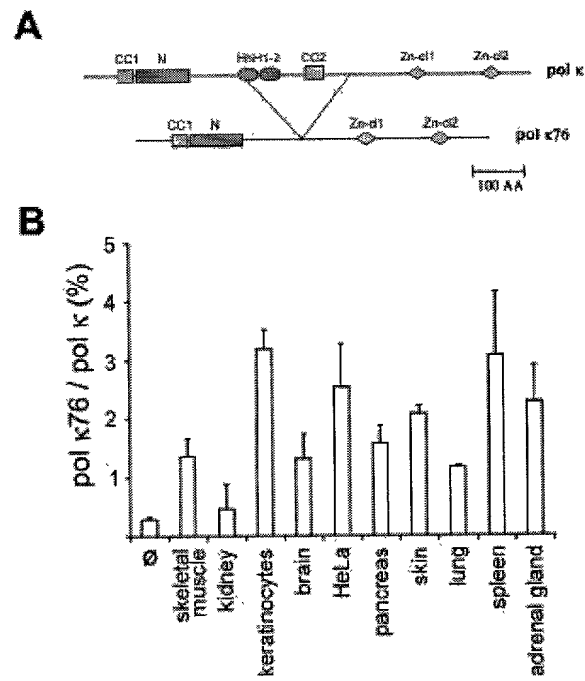


FIGURE 10

